

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: WALLACH, David
BIGDA, Jacek
BELETSKY, Igor
METT, Igor
ENGELMANN, Hartmut
- (ii) TITLE OF INVENTION: TNF INHIBITORS
- (iii) NUMBER OF SEQUENCES: 8
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: BROWDY AND NEIMARK
 - (B) STREET: 419 Seventh Street, N.W.
 - (C) CITY: Washington
 - (D) STATE: D.C.
 - (E) COUNTRY: USA
 - (F) ZIP: 20004
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/476,862
 - (B) FILING DATE: 07-JUN-1995
 - (C) CLASSIFICATION: 514
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: IL 107267
 - (B) FILING DATE: 12-OCT-1993
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: IL 94039
 - (B) FILING DATE: 06-APR-1990
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: IL 91229
 - (B) FILING DATE: 06-AUG-1989
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: IL 90339
 - (B) FILING DATE: 18-MAY-1989
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: BROWDY, Roger L.
 - (B) REGISTRATION NUMBER: 25,618
 - (C) REFERENCE/DOCKET NUMBER: WALLACH=12A
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 202-628-5197
 - (B) TELEFAX: 202-737-3528

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2224 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 90..1472

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGGAGCGCAG CGGAGCCTGG AGAGAAGGCG CTGGGCTGCG AGGGCGCGAG GGCAGCGAGGG	60
CAGGGGGCAA CGGGACCCCG CCCGCACCC ATG GCG CCC GTC GCC GTC TGG GCC Met Ala Pro Val Ala Val Trp Ala	113
1 5	
CGC CTG GCC GTC GGA CTG GAG CTC TGG GCT GCG GCG CAC GCC TTG CCC Ala Leu Ala Val Gly Leu Glu Leu Trp Ala Ala Ala His Ala Leu Pro	161
10 15 20	
GCC CAG GTG GCA TTT ACA CCC TAC GCC CCG GAG CCC GGG AGC ACA TGC Ala Gln Val Ala Phe Thr Pro Tyr Ala Pro Glu Pro Gly Ser Thr Cys	209
25 30 35 40	
CGG CTC AGA GAA TAC TAT GAC CAG ACA GCT CAG ATG TGC TGC AGC AAA Arg Leu Arg Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys Cys Ser Lys	257
45 50 55	
TGC TCG CCG GGC CAA CAT GCA AAA GTC TTC TGT ACC AAG ACC TCG GAC Cys Ser Pro Gly Gln His Ala Lys Val Phe Cys Thr Lys Thr Ser Asp	305
60 65 70	
ACC GTG TGT GAC TCC TGT GAG GAC AGC ACA TAC ACC CAG CTC TGG AAC Thr Val Cys Asp Ser Cys Glu Asp Ser Thr Tyr Thr Gln Leu Trp Asn	353
75 80 85	
TGG GTT CCC GAG TGC TTG AGC TGT GGC TCC CGC TGT AGC TCT GAC CAG Trp Val Pro Glu Cys Leu Ser Cys Gly Ser Arg Cys Ser Ser Asp Gln	401
90 95 100	
GTG GAA ACT CAA GCC TGC ACT CGG GAA CAG AAC CGC ATC TGC ACC TGC Val Glu Thr Gln Ala Cys Thr Arg Glu Gln Asn Arg Ile Cys Thr Cys	449
105 110 115 120	
AGG CCC GGC TGG TAC TGC GCG CTG AGC AAG CAG GAG GGG TGC CGG CTG Arg Pro Gly Trp Tyr Cys Ala Leu Ser Lys Gln Glu Gly Cys Arg Leu	497
125 130 135	
TGC GCG CCG CTG CGC AAG TGC CGC CCG GGC TTC GGC GTG GCC AGA CCA Cys Ala Pro Leu Arg Lys Cys Arg Pro Gly Phe Gly Val Ala Arg Pro	545
140 145 150	
GGA ACT GAA ACA TCA GAC GTG GTG TGC AAG CCC TGT GCC CCG GGG ACG Gly Thr Glu Thr Ser Asp Val Val Cys Lys Pro Cys Ala Pro Gly Thr	593
155 160 165	
TTC TCC AAC ACG ACT TCA TCC ACG GAT ATT TGC AGG CCC CAC CAG ATC Phe Ser Asn Thr Thr Ser Ser Thr Asp Ile Cys Arg Pro His Gln Ile	641
170 175 180	
TGT AAC GTG GTG GCC ATC CCT GGG AAT GCA AGC ATG GAT GCA GTC TGC Cys Asn Val Val Ala Ile Pro Gly Asn Ala Ser Met Asp Ala Val Cys	689
185 190 195 200	
ACG TCC ACG TCC CCC ACC CGG AGT ATG GCC CCA GGG GCA GTA CAC TTA Thr Ser Thr Ser Pro Thr Arg Ser Met Ala Pro Gly Ala Val His Leu	737
205 210 215	

CCC CAG CCA GTG TCC ACA CGA TCC CAA CAC ACG CAG CCA ACT CCA GAA Pro Gln Pro Val Ser Thr Arg Ser Gln His Thr Gln Pro Thr Pro Glu 220 225 230	785
CCC AGC ACT GCT CCA AGC ACC TCC TTC CTG CTC CCA ATG GGC CCC AGC Pro Ser Thr Ala Pro Ser Thr Ser Phe Leu Leu Pro Met Gly Pro Ser 235 240 245	833
CCC CCA GCT GAA GGG AGC ACT GGC GAC TTC GCT CTT CCA GTT GGA CTG Pro Pro Ala Glu Gly Ser Thr Gly Asp Phe Ala Leu Pro Val Gly Leu 250 255 260	881
ATT GTG GGT GTG ACA GCC TTG GGT CTA CTA ATA ATA GGA GTG GTG AAC Ile Val Gly Val Thr Ala Leu Gly Leu Leu Ile Ile Gly Val Val Asn 265 270 275 280	929
TGT GTC ATC ATG ACC CAG GTG AAA AAG AAG CCC TTG TGC CTG CAG AGA Cys Val Ile Met Thr Gln Val Lys Lys Lys Pro Leu Cys Leu Gln Arg 285 290 295	977
GAA GCC AAG GTG CCT CAC TTG CCT GCC GAT AAG GCC CGG GGT ACA CAG Glu Ala Lys Val Pro His Leu Pro Ala Asp Lys Ala Arg Gly Thr Gln 300 305 310	1025
GCC CCC GAG CAG CAG CAC CTG CTG ATC ACA GCG CCG AGC TCC AGC AGC Gly Pro Glu Gln Gln His Leu Leu Ile Thr Ala Pro Ser Ser Ser Ser 315 320 325	1073
AGC TCC CTG GAG AGC TCG GCC AGT GCG TTG GAC AGA AGG GCG CCC ACT Ser Ser Leu Glu Ser Ser Ala Ser Ala Leu Asp Arg Arg Ala Pro Thr 330 335 340	1121
CGG AAC CAG CCA CAG GCA CCA GGC GTG GAG GCC AGT GGG GCC GGG GAG Arg Asn Gln Pro Gln Ala Pro Gly Val Glu Ala Ser Gly Ala Gly Glu 345 350 355 360	1169
GCC CGG GCC AGC ACC GGG AGC TCA GAT TCT TCC CCT GGT GGC CAT GGG Ala Arg Ala Ser Thr Gly Ser Ser Asp Ser Ser Pro Gly Gly His Gly 365 370 375	1217
ACC CAG GTC AAT GTC ACC TGC ATC GTG AAC GTC TGT AGC AGC TCT GAC Thr Gln Val Asn Val Thr Cys Ile Val Asn Val Cys Ser Ser Ser Asp 380 385 390	1265
CAC AGC TCA CAG TGC TCC TCC CAA GCC AGC TCC ACA ATG GGA GAC ACA His Ser Ser Gln Cys Ser Ser Gln Ala Ser Ser Thr Met Gly Asp Thr 395 400 405	1313
GAT TCC AGC CCC TCG GAG TCC CCG AAG GAC GAG CAG GTC CCC TTC TCC Asp Ser Ser Pro Ser Glu Ser Pro Lys Asp Glu Gln Val Pro Phe Ser 410 415 420	1361
AAG GAG GAA TGT GCC TTT CGG TCA CAG CTG GAG ACG CCA GAG ACC CTG Lys Glu Glu Cys Ala Phe Arg Ser Gln Leu Glu Thr Pro Glu Thr Leu 425 430 435 440	1409
CTG GGG AGC ACC GAA GAG AAG CCC CTG CCC CTT GGA GTG CCT GAT GCT Leu Gly Ser Thr Glu Glu Lys Pro Leu Pro Leu Gly Val Pro Asp Ala 445 450 455	1457
GGG ATG AAG CCC AGT TAACCAGGCC GGTGTGGC GTGTCGTAGC CAAGGTGGC Gly Met Lys Pro Ser 460	1512
TGAGCCCTGG CAGGATGACC CTGCGAAGGG GCCCTGGTCC TTCCAGGCC CCACCACTAG GACTCTGAGG CTCTTCTGG GCCAAGTTCC TCTAGTGCCT TCCACAGCCG CAGCCTCCCT	1572 1632

CTGACCTGCA	GGCCAAGAGC	AGAGGCAGCG	AGTTGGGAA	AGCCTCTGCT	GCCATGGTGT	1692
GTCCCTCTCG	GAAGGCTGGC	TGGGCATGGA	CGTTCGGGC	ATGCTGGGC	AAGTCCCTGA	1752
CTCTCTGTGA	CCTGCCCGC	CCAGCTGCAC	CTGCCAGCCT	GGCTTCTGGA	GCCCTTGGGT	1812
TTTTGTTTG	TTTGTGTTGTT	TGTTGTTG	TTTCTCCCCC	TGGGCTCTGC	CCAGCTCTGG	1872
CTTCCAGAAA	ACCCCAGCAT	CCTTTCTGC	AGAGGGCTT	TCTGGAGAGG	AGGGATGCTG	1932
CCTGAGTCAC	CCATGAAAGAC	AGGACAGTGC	TTCAGCCTGA	GGCTGAGACT	GCAGGGATGGT	1992
CCTGGGGCTC	TGTGTAGGGA	GGAGGTGGCA	GCCCTGTAGG	GAACGGGGTC	CTTCAAGTTA	2052
GCTCAGGAGG	CTTGGAAAGC	ATCACCTCAG	GCCAGGTGCA	GTGGCTCACG	CCTATGATCC	2112
CAGCACTTTG	GGAGGCTGAG	GCGGGTGGAT	CACCTGAGGT	TAGGAGTTCG	AGACCAGCCT	2172
GGCCAACATG	GTAAAACCCC	ATCTCTACTA	AAAATACAGA	AATTAGCCGG	GC	2224

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 461 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Ala	Pro	Val	Ala	Val	Trp	Ala	Ala	Leu	Ala	Val	Gly	Leu	Glu	Leu
1				5					10					15	
Trp	Ala	Ala	Ala	His	Ala	Leu	Pro	Ala	Gln	Val	Ala	Phe	Thr	Pro	Tyr
				20				25					30		
Ala	Pro	Glu	Pro	Gly	Ser	Thr	Cys	Arg	Leu	Arg	Glu	Tyr	Tyr	Asp	Gln
				35			40				45				
Thr	Ala	Gln	Met	Cys	Cys	Ser	Lys	Cys	Ser	Pro	Gly	Gln	His	Ala	Lys
			50			55				60					
Val	Phe	Cys	Thr	Lys	Thr	Ser	Asp	Thr	Val	Cys	Asp	Ser	Cys	Glu	Asp
				65		70			75				80		
Ser	Thr	Tyr	Thr	Gln	Leu	Trp	Asn	Trp	Val	Pro	Glu	Cys	Leu	Ser	Cys
				85			90					95			
Gly	Ser	Arg	Cys	Ser	Ser	Asp	Gln	Val	Glu	Thr	Gln	Ala	Cys	Thr	Arg
			100				105					110			
Glu	Gln	Asn	Arg	Ile	Cys	Thr	Cys	Arg	Pro	Gly	Trp	Tyr	Cys	Ala	Leu
			115				120				125				
Ser	Lys	Gln	Glu	Gly	Cys	Arg	Leu	Cys	Ala	Pro	Leu	Arg	Lys	Cys	Arg
			130			135				140					
Pro	Gly	Phe	Gly	Val	Ala	Arg	Pro	Gly	Thr	Glu	Thr	Ser	Asp	Val	Val
				145		150			155				160		
Cys	Lys	Pro	Cys	Ala	Pro	Gly	Thr	Phe	Ser	Asn	Thr	Thr	Ser	Thr	
				165			170					175			

Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly
 180 185 190
 Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser
 195 200 205
 Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser
 210 215 220
 Gln His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser
 225 230 235 240
 Phe Leu Leu Pro Met Gly Pro Ser Pro Ala Glu Gly Ser Thr Gly
 245 250 255
 Asp Phe Ala Leu Pro Val Gly Leu Ile Val Gly Val Thr Ala Leu Gly
 260 265 270
 Leu Leu Ile Ile Gly Val Val Asn Cys Val Ile Met Thr Gln Val Lys
 275 280 285
 Lys Lys Pro Leu Cys Leu Gln Arg Glu Ala Lys Val Pro His Leu Pro
 290 295 300
 Ala Asp Lys Ala Arg Gly Thr Gln Gly Pro Glu Gln Gln His Leu Leu
 305 310 315 320
 Ile Thr Ala Pro Ser Ser Ser Ser Ser Leu Glu Ser Ser Ala Ser
 325 330 335
 Ala Leu Asp Arg Arg Ala Pro Thr Arg Asn Gln Pro Gln Ala Pro Gly
 340 345 350
 Val Glu Ala Ser Gly Ala Gly Glu Ala Arg Ala Ser Thr Gly Ser Ser
 355 360 365
 Asp Ser Ser Pro Gly Gly His Gly Thr Gln Val Asn Val Thr Cys Ile
 370 375 380
 Val Asn Val Cys Ser Ser Ser Asp His Ser Ser Gln Cys Ser Ser Gln
 385 390 395 400
 Ala Ser Ser Thr Met Gly Asp Thr Asp Ser Ser Pro Ser Glu Ser Pro
 405 410 415
 Lys Asp Glu Gln Val Pro Phe Ser Lys Glu Glu Cys Ala Phe Arg Ser
 420 425 430
 Gln Leu Glu Thr Pro Glu Thr Leu Leu Gly Ser Thr Glu Glu Lys Pro
 435 440 445
 Leu Pro Leu Gly Val Pro Asp Ala Gly Met Lys Pro Ser
 450 455 460

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 153 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Val Cys Pro Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser Ile Cys
 1 5 10 15

Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly
 20 25 30

Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr
 35 40 45

Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser Lys Cys Arg
 50 55 60

Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp Arg Asp
 65 70 75 80

Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu
 85 90 95

Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu Asn Gly Thr Val
 100 105 110

His Leu Ser Cys Gln Glu Lys Gln Asn Thr Val Cys Thr Cys His Ala
 115 120 125

Gly Phe Phe Leu Arg Glu Asn Glu Cys Val Ser Cys Ser Asn Cys Lys
 130 135 140

Lys Ser Leu Glu Cys Thr Lys Leu Cys
 145 150

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 163 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys Cys
 1 5 10 15

Ser Lys Cys Ser Pro Gly Gln His Ala Lys Val Phe Cys Thr Lys Thr
 20 25 30

Ser Asp Thr Val Cys Asp Ser Cys Glu Asp Ser Thr Tyr Thr Gln Leu
 35 40 45

Trp Asn Trp Val Pro Glu Cys Leu Ser Cys Gly Ser Arg Cys Ser Asp
 50 55 60

Asp Gln Val Glu Thr Gln Ala Cys Thr Arg Glu Gln Asn Arg Ile Cys
 65 70 75 80

Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu Ser Lys Gln Glu Gly Cys
 85 90 95

Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg Pro Gly Phe Gly Val Ala
 100 105 110

Arg Pro Gly Thr Glu Thr Ser Asp Val Val Cys Lys Pro Cys Ala Pro
 115 120 125

Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr Asp Ile Cys Arg Pro His
 130 135 140
 Gln Ile Cys Asn Val Val Ala Ile Pro Gly Asn Ala Ser Met Asp Ala
 145 150 155 160
 Val Cys Thr

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Gln Asn Leu Glu Gly Leu His His Asp Gly Gln Phe Cys His Lys Pro
 1 5 10 15
 Cys Pro Pro Gly Glu Arg Lys Ala Arg Asp Cys Thr Val Asn Gly Asp
 20 25 30
 Glu Pro Asp Cys Val Pro Cys Gln Glu Gly Lys Glu Tyr Thr Asp Lys
 35 40 45
 Ala His Phe Ser Ser Lys Cys Arg Arg Cys Arg Leu Cys Asp Glu Gly
 50 55 60
 His Gly Leu Glu Val Glu Ile Asn Cys Thr Arg Thr Gln Asn Thr Lys
 65 70 75 80
 Cys Arg Cys Lys Pro Asn Phe Phe Cys Asn Ser Thr Val Cys Glu His
 85 90 95
 Cys Asp Pro Cys Thr Lys Cys Glu His Gly Ile Ile Lys Glu Cys Thr
 100 105 110
 Leu Thr Ser Asn Thr Lys Cys
 115

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Ala Cys Pro Thr Gly Leu Tyr Thr His Ser Gly Glu Cys Cys Lys Ala
 1 5 10 15
 Cys Asn Leu Gly Glu Gly Val Ala Gln Pro Cys Gly Ala Asn Gln Thr
 20 25 30
 Val Cys Glu Pro Cys Leu Asp Ser Val Thr Ser Ser Asp Val Val Ser
 35 40 45

Ala Thr Glu Pro Cys Lys Pro Cys Thr Glu Cys Val Gly Leu Gln Ser
 50 55 60

His Ser Ala Pro Cys Val Glu Ala Asp Asp Ala Val Cys Arg Cys Ala
 65 70 75 80

Tyr Gly Tyr Tyr Gln Asp Glu Thr Thr Gly Arg Cys Glu Ala Cys Arg
 85 90 95

Val Cys Glu Ala Gly Ser Gly Leu Val Phe Ser Cys Gln Asp Lys Gln
 100 105 110

Asn Thr Val Cys Glu Glu Cys Pro Asp Gly Thr Tyr Ser Asp Glu Ala
 115 120 125

Asn His Val Asp Pro Cys Leu Pro Cys Thr Val Cys Glu Asp Thr Glu
 130 135 140

Arg Gln Leu Arg Glu Cys Thr Arg Trp Ala Asp Ala Glu Cys Glu
 145 150 155

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 162 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Ala Cys Arg Glu Lys Gln Tyr Leu Ile Asn Ser Gln Cys Cys Ser Leu
 1 5 10 15

Cys Gln Pro Gly Gln Lys Leu Val Ser Asp Cys Thr Glu Phe Thr Glu
 20 25 30

Thr Glu Cys Leu Pro Cys Gly Glu Ser Glu Phe Leu Asp Thr Trp Asn
 35 40 45

Arg Glu Thr His Cys His Gln His Lys Tyr Cys Asp Pro Asn Leu Gly
 50 55 60

Leu Arg Val Gln Gln Lys Gly Thr Ser Glu Thr Asp Thr Ile Cys Thr
 65 70 75 80

Cys Glu Glu Gly Trp His Cys Thr Ser Glu Ala Cys Glu Ser Cys Val
 85 90 95

Leu His Arg Ser Cys Ser Pro Gly Phe Gly Val Lys Gln Ile Ala Thr
 100 105 110

Gly Val Ser Asp Thr Ile Cys Glu Pro Cys Pro Val Gly Phe Phe Ser
 115 120 125

Asn Val Ser Ser Ala Phe Glu Lys Cys His Pro Thr Ser Cys Glu Thr
 130 135 140

Lys Asp Leu Val Val Gln Gln Ala Gly Thr Asn Lys Thr Asp Val Val
 145 150 155 160

Cys Gly

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 140 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Asn Cys Val Lys Asp Thr Tyr Pro Ser Gly His Lys Cys Cys Arg Glu
1 5 10 15

Cys Gln Pro Gly His Gly Met Val Ser Arg Cys Asp His Thr Arg Asp
20 25 30

Thr Val Cys His Pro Cys Glu Pro Gly Phe Tyr Asn Glu Ala Val Asn
35 40 45

Tyr Asp Thr Cys Lys Gln Cys Thr Gln Cys Asn His Arg Ser Gly Ser
50 55 60

Glu Leu Lys Gln Asn Cys Thr Pro Thr Glu Asp Thr Val Cys Gln Cys
65 70 75 80

Arg Pro Gly Thr Gln Pro Arg Gln Asp Ser Ser His Lys Leu Gly Val
85 90 95

Asp Cys Val Pro Cys Pro Pro Gly His Phe Ser Pro Gly Ser Asn Gln
100 105 110

Ala Cys Lys Pro Trp Thr Asn Cys Thr Leu Ser Gly Lys Gln Ile Arg
115 120 125

His Pro Ala Ser Asn Ser Leu Asp Thr Val Cys Glu
130 135 140